IN THE CLAIMS:

Please amend the claims as follows. A marked-up copy of the claims is included as an attachment pursuant to 37 C.F.R. §1.121.

1.(Amended) A process for presenting passenger peptides or polypeptides on the surface of Gram-negative host bacteria, comprising

a) providing a host bacterium transformed with a vector encoding a polynucleotide operatively linked to a promoter, wherein said polynucleotide comprises:

(i) a nucleotide sequence encoding a signal peptide,

(ii) a nucleotide sequence encoding a passenger peptide or polypeptide,

(iii) a nucleotide sequence encoding a protease recognition site,

(iv) a nucleotide sequence encoding a transmembrane linker, and

(v) a nucleotide sequence encoding a transporter domain of an autotransporter; and

b) cultivating the host bacterium under conditions for inducing expression of the polynucleotide and presentation of the passenger peptide or polypeptide of step (ii) on the surface of the host bacterium, wherein the passenger peptide or polypeptide of step (ii) is heterologous in relation to the transporter domain of step (v), and the host bacterium is homologous in relation to the transporter domain of step (v).

2. (Amended) The process according to claim 1, wherein the autotransporter is from a bacterium of genus enterobacterioceae.

3. (Twice Amended) The process according to claim 1, wherein the transporter domain is an Aida protein of E. coli or a variant thereof.

4. (Twice Amended) The process according to claim 1, wherein the transporter domain is an SepA protein of Shigella flexneri or a variant thereof.

5. (Twice Amended) The process according to claim 1, wherein the transporter domain is an IcsA protein of Shigella flexneri or a variant thereof.

6. (Amended) The process according to claim 2, wherein the transporter domain is a Tsh protein of E. coli or a variant thereof.

7. (Amended) The process according to claim 2, wherein the transporter domain is an Ssp protein of Serratia marcescens or a variant thereof.

8. (Amended) The process according to claim 1, wherein the transporter domain is an Hsr protein of Helicobacter mustelae, a Prn protein of Bordetella ssp., a Hap protein of Haemophilus influenzae, a BrkA protein of Bordetella pertussis, a VacA protein of Helicobacter pylori or any one of a rickettsial-derived protein comprising a 190kDa cell surface protein, SpaP, r0mpB or S1pT.

9. (Twice Amended) The process according to claim 1, wherein one or more peptides have a length of 4-50 amino acids.

10. (Twice Amended) The process according to claim 1, wherein one or more polypeptides are of eukaryotic origin.

11. (Amended) The process according to claim 10, wherein the passenger polypeptide is an antibody or an antigen-binding domain of an antibody.

12. (Amended) The process according to claim 10, wherein the passenger polypeptide is the α chain of an MHC class II molecule.

13. (Amended) The process according to claim 10, wherein the passenger polypeptide is the β chain of an MHC class II molecule.

14. (Amended) The process according to claim 13, wherein the passenger polypeptide is the β chain of an MHC class II molecule comprising an N terminus capable of folding into the binding cavity of a functional MHC molecule.

15. (Twice Amended) The process according to claim 1, wherein libraries of variant passenger peptides or polypeptides are expressed in host cells and presented on the host cell-surface.

16. (Amended) The process according to claim 15, wherein the variant passenger peptides or polypeptides are presented with a mixture of non-variant passenger polypeptides.

17. (Twice Amended) The process according to claim 1, wherein a host bacterial cell presents different passenger peptides or polypeptides connected to a transporter domain.

18. (Amended) The process according to claim 17, comprising different transporter domains and different passenger peptides or polypeptides.

19. (Twice Amended) The process according to claim 15, further comprising a step of selecting single passenger peptides or polypeptides from a library of variant peptides or polypeptides.

41.(Amended) A process for obtaining a library of bacteria expressing a variant population of surface-exposed passenger peptides or polypeptides, the process comprising:

a) providing at least one vector comprising a chimeric gene obtained by cloning in frame, a nucleotide sequence encoding a signal peptide, a nucleotide

sequence encoding a passenger peptide or polypeptide, and a nucleotide sequence encoding a transporter domain for an AIDA protein of *E. coli* or a variant thereof;

b) mutagenizing the at least one vector to introduce variation into the nucleotide sequence encoding the passenger peptide or polypeptide;

c) transfecting the at least one vector of step (b) into host bacteria capable of stably presenting the passenger peptide or polypeptide on the cell surface;

d) expressing the chimeric gene in the host bacteria;

e) culturing the host bacteria of step (d) to produce the passenger peptide or polypeptide stably exposed on the cell surface;

f) selecting the host bacteria of step (e) with a surface-exposed passenger peptide or polypeptide,

g) identifying and characterizing a binding partner for the surface-exposed passenger peptide or polypeptide, and

wherein the process is repeated several times in order to obtain the library of bacteria expressing the variant population of surface-exposed passenger peptides or polypeptides.

Please cancel claim 42 without prejudice or disclaimer.

43.(Amended) The process according to claim 41, wherein the passenger peptides or polypeptides have an affinity for a binding partner selected from the group consisting of a ligand, a receptor, an antigen, a toxin-binding protein, a protein with enzymatic

activity, a nucleic acid-binding protein, an inhibitor, a protein having chelator properties, an antibody and an antigen-binding domain of an antibody.

44. (Twice Amended) The process according to claim 1, wherein the bacteria expressing the surface-exposed passenger peptides or polypeptides have a binding affinity identified by binding to a labeled or unlabeled immobilized binding partner.

45.(Amended) The process according to claim 41, comprising introducing a modification into the binding partner of step g) wherein the modification is detected between steps g) and h) by a binding partner specific for the modification.

46.(Twice Amended) The process according to claim 41, wherein the passenger peptide or polypeptide is chemically or enzymatically modified on the bacterial surface.

47.(Twice Amended) The process according to claim 46, wherein the modification is a non-covalent modification.

48.(Twice Amended) The process according to claim 46, wherein the modification is a covalent modification.

49.(Twice Amended) The process according to claim 48, wherein the modification is a glycosylation.

50.(Twice Amended) The process according to claim 48, wherein the modification is a phosphorylation.

51.(Twice Amended) The process according to claim 46, wherein the modification is a proteolysis.

52.(Twice Amended) The process according to claim 51, wherein the passenger peptides or polypeptides are selectively released from the bacterial surface by endogenous or exogenous proteases.

53.(Twice Amended) The process according to claim 52, wherein the passenger peptides or polypeptides are released by an endogenous protease of the host cell comprising OmpT protease, OmpK protease or protease X.

54.(Twice Amended) The process according to claim 53, wherein the passenger peptides or polypeptides are released by an exogenous protease comprising IgA protease, thrombin or factor X.

55.(Amended) A recombinant vector encoding a chimeric polynucleotide operatively linked to a promoter, the chimeric polynucleotide comprising:

a) a nucleotide sequence encoding a signal peptide,

b) a nucleotide sequence encoding a passenger peptide or polypeptide,

c) a nucleotide sequence encoding a protease recognition site,

d) a nucleotide sequence encoding a transmembrane linker, and

e) a nucleotide sequence encoding a transporter domain for an AIDA protein of *E. coli* or a variant thereof;

wherein the nucleotide sequence encoding the passenger peptide or polypeptide of step b) is heterologous in relation to the nucleotide sequence encoding the transporter domain of step e).

56.(Amended) A recombinant Gram-negative host bacterium, wherein the bacterium is transformed with a vector according to claim 55.

57.(Amended) A recombinant Gram-negative host bacterium transformed with a recombinant vector encoding a chimeric polynucleotide operatively linked to a promoter, the chimeric polynucleotide comprising:

a) a nucleotide sequence encoding a signal peptide,

b) a nucleotide sequence encoding a passenger peptide or polypeptide,

c) a nucleotide sequence encoding a protease recognition site,

d) a nucleotide sequence encoding a transmembrane linker, and

e) a nucleotide sequence encoding a transporter domain of an autotransporter;

wherein the nucleotide sequence encoding the passenger peptide or polypeptide of step b) is heterologous in relation to the nucleotide sequence encoding the transporter domain of step e), and wherein the host bacterium is homologous in relation to the nucleotide sequence encoding the transporter domain of step e).

58.(Amended) The host bacterium according to claim 57, wherein the bacterium is an *E. coli* cell.

59.(Amended) The host bacterium according to claim 57, wherein the nucleotide of step e) encodes a transporter domain for an AIDA protein or a variant thereof.

REMARKS

The Office Action of January 3, 2002 has been received and carefully reviewed and the foregoing amended claims and the following comments are a complete response thereto.

Claims 1-19 and 41-59 are all the pending claims for this application. Claims 1-3, 9-19 and 41-59 are the claims under examination and Claims 1-19 and 41-59 have been amended to introduce cosmetic changes, none of which narrow the scope of the claims. Claim 42 has been canceled without prejudice or disclaimer.